

Jose A Navas-Molina

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/9381723/publications.pdf>

Version: 2024-02-01

16
papers

18,469
citations

567281

15
h-index

839539

18
g-index

22
all docs

22
docs citations

22
times ranked

21886
citing authors

#	ARTICLE	IF	CITATIONS
1	Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. Nature Biotechnology, 2019, 37, 852-857.	17.5	11,167
2	Phylogenetic Placement of Exact Amplicon Sequences Improves Associations with Clinical Information. MSystems, 2018, 3, .	3.8	376
3	Qiita: rapid, web-enabled microbiome meta-analysis. Nature Methods, 2018, 15, 796-798.	19.0	459
4	Balance Trees Reveal Microbial Niche Differentiation. MSystems, 2017, 2, .	3.8	284
5	Bringing the Dynamic Microbiome to Life with Animations. Cell Host and Microbe, 2017, 21, 7-10.	11.0	95
6	Deblur Rapidly Resolves Single-Nucleotide Community Sequence Patterns. MSystems, 2017, 2, .	3.8	1,339
7	A communal catalogue reveals Earth's multiscale microbial diversity. Nature, 2017, 551, 457-463.	27.8	1,942
8	Correcting for Microbial Blooms in Fecal Samples during Room-Temperature Shipping. MSystems, 2017, 2, .	3.8	116
9	Inflammation-induced IgA+ cells dismantle anti-liver cancer immunity. Nature, 2017, 551, 340-345.	27.8	396
10	The microbiome and big data. Current Opinion in Systems Biology, 2017, 4, 92-96.	2.6	11
11	From Sample to Multi-Omics Conclusions in under 48 Hours. MSystems, 2016, 1, .	3.8	53
12	The Oral and Skin Microbiomes of Captive Komodo Dragons Are Significantly Shared with Their Habitat. MSystems, 2016, 1, .	3.8	61
13	Open-Source Sequence Clustering Methods Improve the State Of the Art. MSystems, 2016, 1, .	3.8	155
14	Subsampled open-reference clustering creates consistent, comprehensive OTU definitions and scales to billions of sequences. PeerJ, 2014, 2, e545.	2.0	535
15	Addressing memory exhaustion failures in Virtual Machines in a cloud environment. , 2013, , .		2
16	Advancing Our Understanding of the Human Microbiome Using QIIME. Methods in Enzymology, 2013, 531, 371-444.	1.0	553